CREST

Genetic Improvement of Data gives double precision invsqrt $\frac{1}{\sqrt{x}}$

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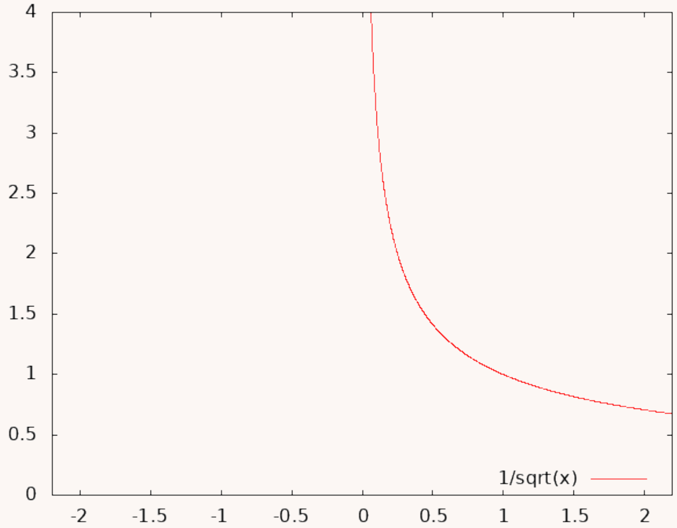
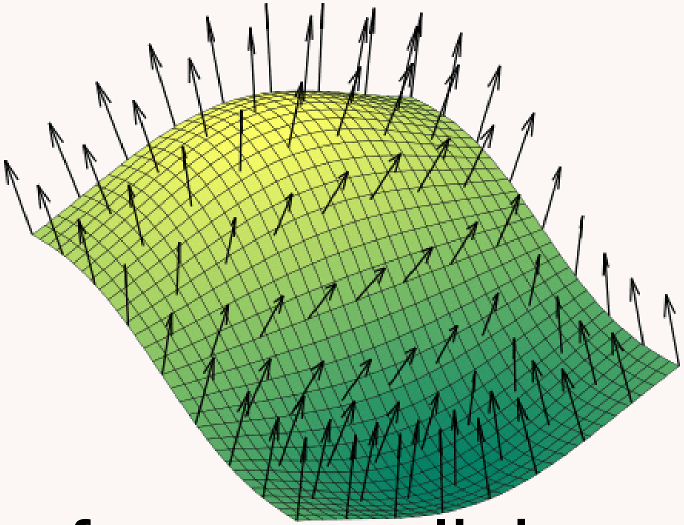
Fluid Genetic Improvement Programming

- Invsqrt $\frac{1}{\sqrt{x}}$ inverted square root
- New type of Genetic Improvement
- Update fluid embedded literals i.e. data
  1. New functionality
  2. Better non-functionality (e.g. faster)?
- Why
  1. FGIP is a new way to do GI, tackle data driven code
  2. Minimal code changes may be more acceptable?

Why invsqrt $\frac{1}{\sqrt{x}}$





- Reciprocal of square root for normalising vectors. E.g. in games, image processing and neural networks
- Before hardware support in GPU invsqrt was computationally heavy. Hence Quake used own approximation, Quare root.

FGIP New type of Genetic Improvement

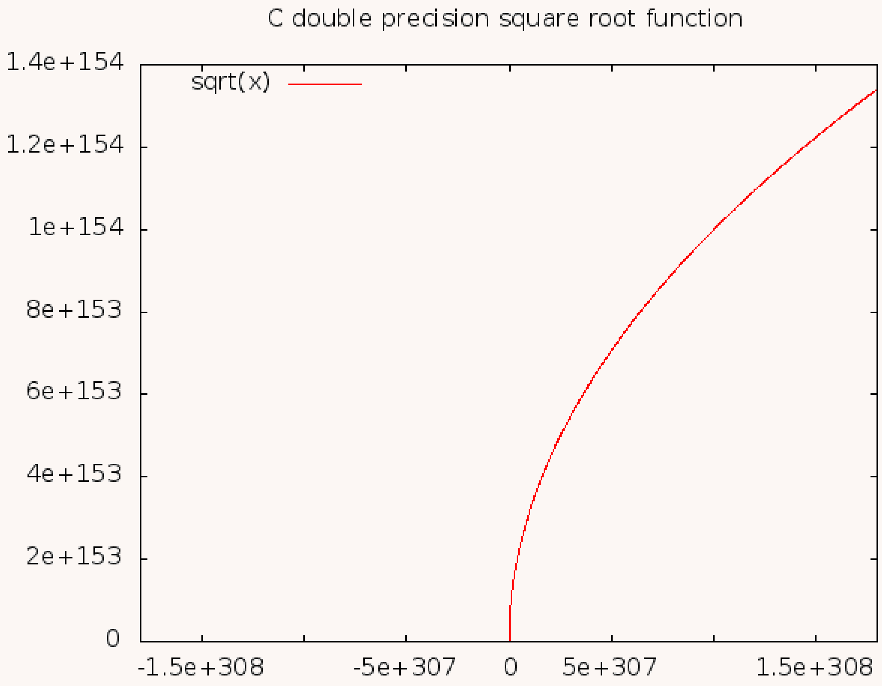
- New functionality via data changes
  - RNAfold better predictions
  - New maths functions, e.g. convert √x into $\frac{1}{\sqrt{x}}$
- Can we do non-functionality (e.g. faster)?
- How is this different from:
  - Deep parameter tuning? Change functionality
    - No mutation testing
    - Emphasis on data rather than values in code
    - Scale: hundreds even thousands of values
    - Multiple examples

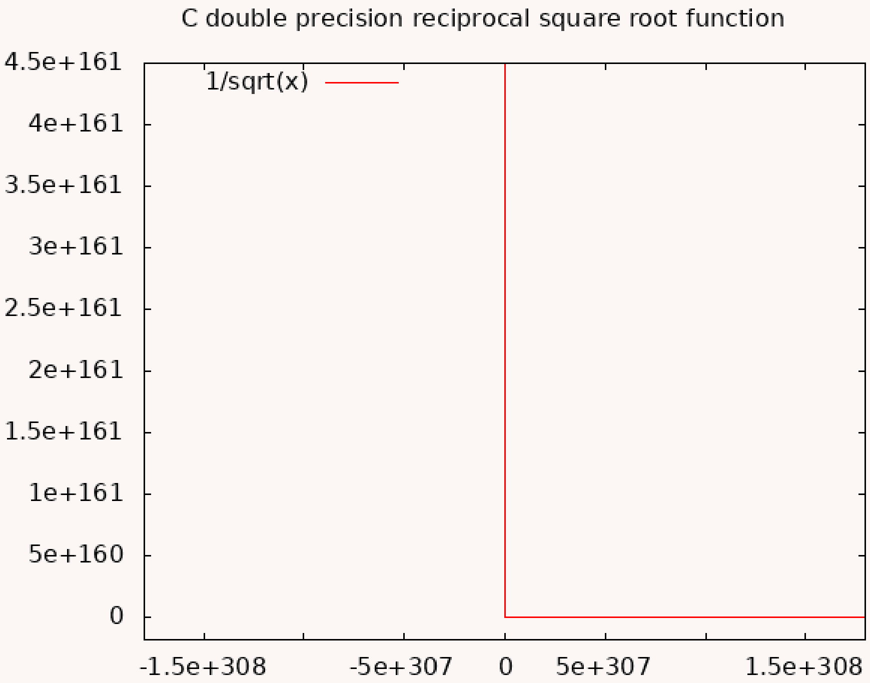
Maintaining Embedded Constants

- EuroGP 2018
  - RNAfold 7000 lines of code 50000 numbers
  - On average better predictions of RNA folding.
  - Shipped since 2.4.7
- CMA-ES evolves data in a GNU C library sqrt to give new functionality with double precision accuracy. sqrt converted to
  - cube root, cbrt
  - square root converted to $\log_2$ (poster monday)
  - invsqrt $\frac{1}{\sqrt{x}}$
  - division less division

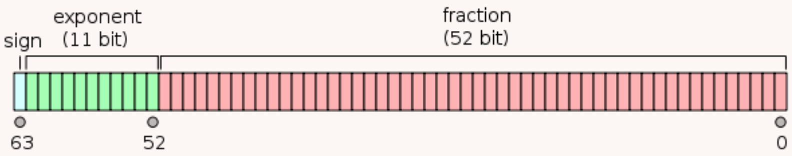
Use CMA-ES to convert sqrt into $\frac{1}{\sqrt{x}}$

By updating table of 512 floats





IEEE 754 Double Precision



GNU C library sqrt converted to $\frac{1}{\sqrt{x}}$

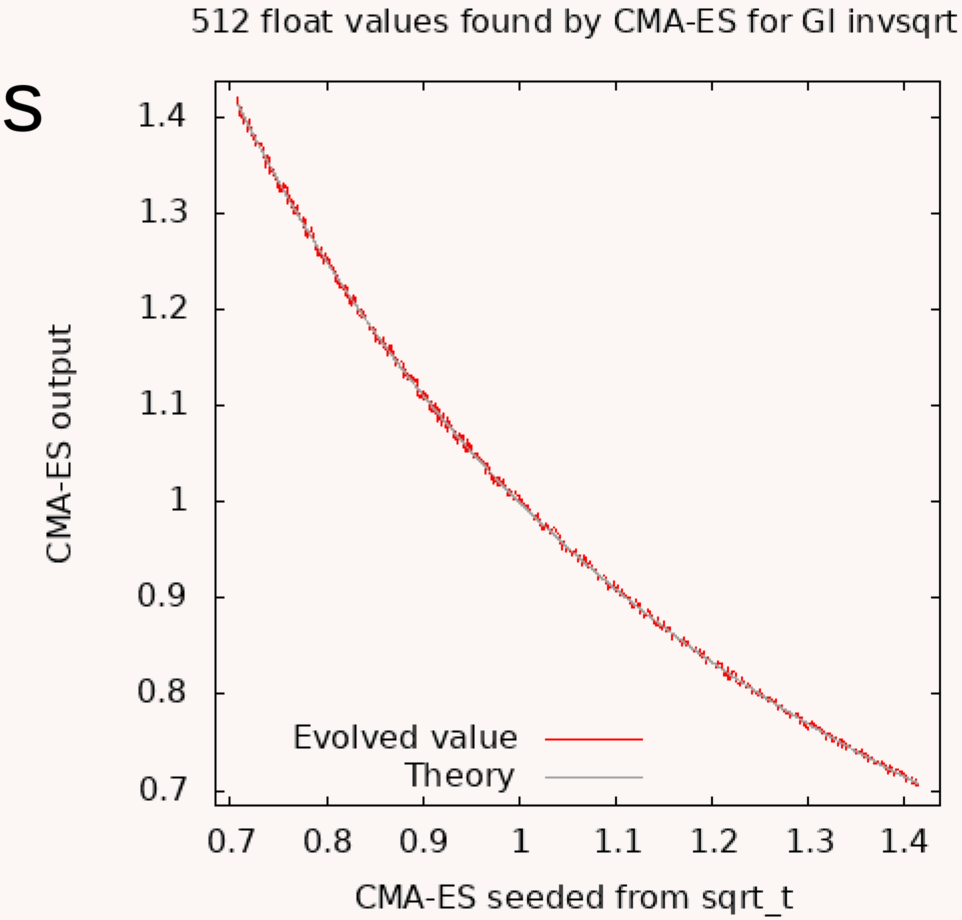
- Chosen implementation of sqrt divides normalised input into 512 bins.
- Each bin holds start point for Newton-Raphson and initial derivative (two floats)
- Run CMA-ES per table element:
  - Seed with square root value, ignore 2nd float
  - Run code with CMA-ES generated test value
  - Fitness = log |1/(c*c) - x| where c=‘invsqrt’(x)

    x takes three test values: smallest, mid, max in bin
  - Random restart if search fails to find value for which 3 diffs are smallest possible

CMA-ES

sqrt seed values close to invsqrt

Evolved value very close to theory.



Evolved $\frac{1}{\sqrt{x}}$

Evolved cbrt tested many thousands of times

- Always within DBL_EPSILON
- Almost always gives best possible double

Compared to Quake (single precision approximation)

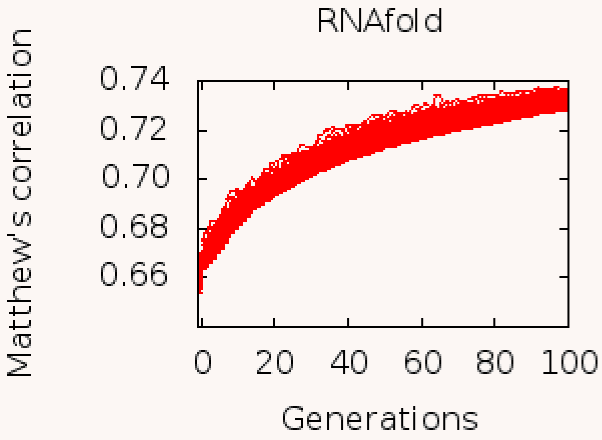
- Quake seldom gives exact answer
- Quake can be 0.17% wrong (0.43/256)
- Quake does not trap negative numbers, sometimes fails, sometimes just wrong
- Quake odd behaviour <1.5 10^{-37} or >3.3 10^{38}

Automatic Software Maintenance

- In a world addicted to software, maintenance is the dominant cost of computing.
- Need to keep parameters up to date. E.g.
  - New science, new laws or regulations, new users, new user expectations
  - Change of load, new hardware (e.g. bigger RAM), automatic porting
  - Search can be fast (total CMA-ES runtime 6 secs)
- Little SBSE research
- Great scope for automation

Summary: FGIP

- Problem of maintaining data in code ignored
- GI can optimize data in programs
- Rapidly generated maths (cbrt, $\log_2$, $\frac{1}{\sqrt{x}}$, $1/x$)
  - Frame work open to evolve new functions
    http://www.cs.ucl.ac.uk/staff/W.Langdon/ftp/gp-code/gi_cbrt.tar.gz
- Software is not fragile



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http://www.cs.ucl.ac.uk/staff/W.Langdon/ http://www.epsrc.ac.uk/

Genetic Programming

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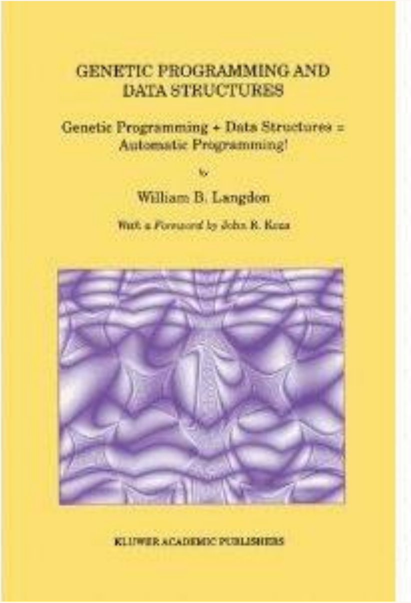

GENETIC PROGRAMMING AND
DATA STRUCTURES

Genetic Programming + Data Structures =
Automatic Programming!

by

William B. Langdon

With a Foreword by John R. Koza

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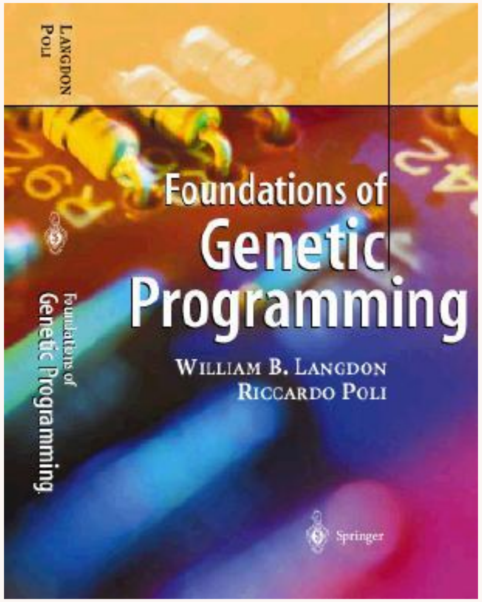

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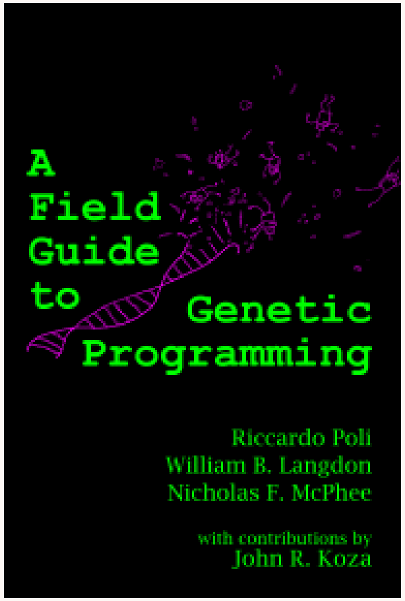


A
Field
Guide
to
Genetic
Programming

Riccardo Poli
William B. Langdon
Nicholas F. McPhee

with contributions by
John R. Koza

Improving RNAfold parameters

EuroGP-2018

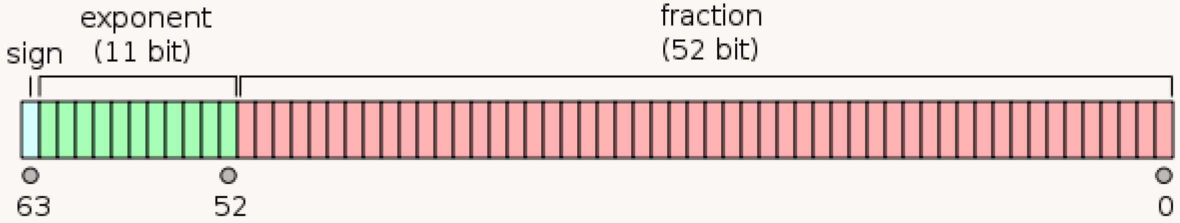
- RNAfold 7100 lines of C source code, 51521 parameters.
- Fitness correlation between prediction and true structure (MCC).
- Post evolution tidy
- 14732 (29%) parameters changed
- Holdout set significant increase in MCC
- Also better than constrained optimisation
- GI parameters rna_langdon2018.par shipped with ViennaRNA since 13 Jun 2018

Manual Changes I

- Most implementations of square root use hardware support.
- GNU C library glibc 2.29 also includes Newton-Raphson iterative solution
- Trap bad values, e.g. negative
- Normalise double input to 0.5 .. 2.0
- Guaranteed convergence in three steps:
  - Update both estimate of √x and derivative
- Apply square root to exponent, ie divide by 2

Code Changes II

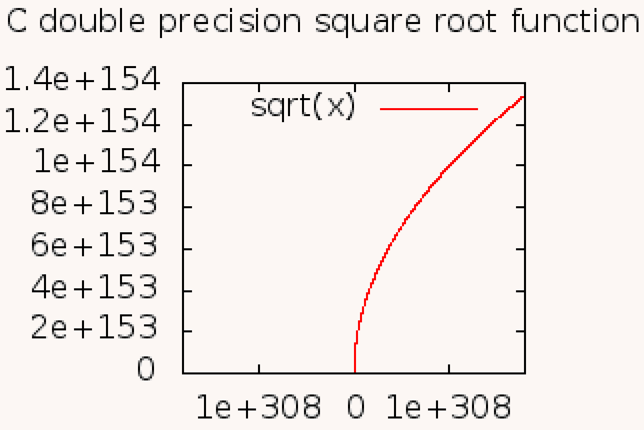
- Normalise double precision input to 1.0..2
  - – Update estimate of $x^{-1/2}$
  - – Use reciprocal of derivative, i.e. $x^3/2$, directly
- Apply invsqrt to exponent, i.e. divide by 2 and make negative.
- Could we use code GI to further improve?

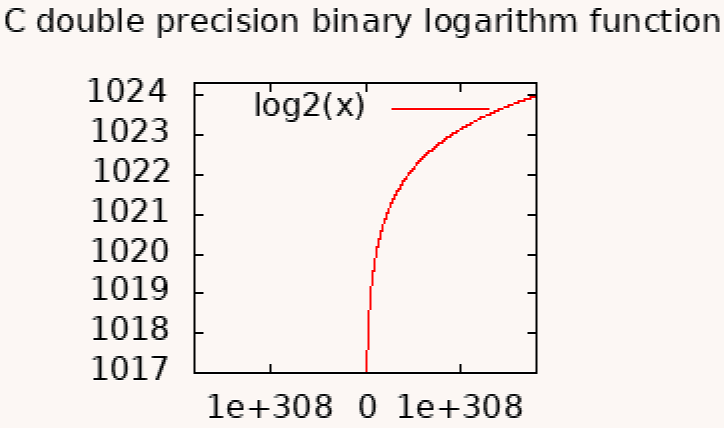


Square root to binary log GECCO-2019

Frame work as sqrt to cbrt but

- Derivative known
- CMA-ES one dimension at a time (512 times) very easy





The Genetic Programming Bibliography

http://gpbib.cs.ucl.ac.uk/

13217 references, 12000 authors

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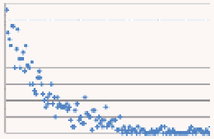

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